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The diversity and structure of populations of *Magnaporthe grisea*, the main fungal pathogen of rice, was described in many countries during the last 20 years. The expected clonal structure of the populations has been illustrated in many studies. The relationship between the genetic structure, deduced from neutral molecular markers, and the pathotypic structure, showed a range of situations varying from a one lineage-one race to almost a one genotype-one race correspondence. These studies have helped in choosing appropriate isolates for genetic characterization and to propose strategies to breed for durable resistance to blast disease. This background information is the basis to understand rice blast population evolution. But, to date, our understanding of how new virulent races appear and spread is limited. For example, the relative importance of short and long distance migration in the spreading of new virulent races is unknown. However, this information is needed to determine at which scale the deployment of a resistance strategy is likely to be effective and durable.

We recently developed and used a set of 18 microsatellite markers for population studies (Adreit et al. *in press* in Molecular Ecology Notes). Preliminary studies on populations from the Central part of Madagascar show that some populations are differentiated at a local scale (1-5 km). These results suggest limited migration.

We also studied the distribution of the genotypes of the cloned avirulence gene ACE1 at the worldwide scale. We determined the ACE1 genotype of more than 800 isolates. Avirulent isolates were the most frequent, were sampled all over the world, and shared the same ACE1 allele. Two major virulent genotypes were identified. Their frequencies vary with geographic origin. These genotypes appeared by a complex duplication/deletion event of ACE1. These two genotypes are widely distributed over different continents. Altogether, these results suggest a unique selection event followed by long distance migration(s).

Our apparently contradictory results from studies at two different geographic scales are explained by two distinct modes of dissemination. Structuration at a local scale is consistent with short distance spore dispersal (1-5 m) observed during natural epidemics. Long distance migrations, including intercontinental, are possible through the transport of infected materials (probably seeds).

Keywords: rice blast, *Magnaporthe*, migration, avirulence

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